

SEQUENCE LISTING

<110> Shionogi & Co., Ltd

<120> Drug for inhibiting myometrial contraction.

<130> S0043PCT

<140>

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<150> JP P1999-177548

<151> 1999-06-23

<150> JP P2000-79171

<151> 1999-03-21

<160> 6

<170> PatentIn Ver. 2.0

<210> 1

<211> 1457

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (165)..(719)

<220>

<221> mat peptide

<222> (447)..(602)

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tggcagatc actctcttag cagggctctgc gcttcgcagc cggg atg aag ctg gtt 176

Met Lys Leu Val

tcc gtc gcc ctg atg tac ctg ggt tgc ctc gcc ttc cta ggc gct gac 224

Ser Val Ala Leu Met Tyr Leu Gly Ser Leu Ala Phe Leu Gly Ala Asp

-90 -85 -80 -75

acc gct cgg ttg gat gtc gcg tgc gag ttt cga aag aag tgg aat aag 272

Thr Ala Arg Leu Asp Val Ala Ser Glu Phe Arg Lys Lys Trp Asn Lys

-70 -65 -60

tgg gct ctg agt cgt ggg aag agg gaa ctg cgg atg tcc agc agc tac 320

Trp Ala Leu Ser Arg Gly Lys Arg Glu Leu Arg Met Ser Ser Ser Tyr

-55 -50 -45

ccc acc ggg ctc gct gac gtg aag gcc ggg cct gcc cag acc ctt att 368

Pro Thr Gly Leu Ala Asp Val Lys Ala Gly Pro Ala Gln Thr Leu Ile

-40 -35 -30

cgg ccc cag gac atg aag ggt gcc tct cga agc ccc gaa gac agc agt 416

Arg Pro Gln Asp Met Lys Gly Ala Ser Arg Ser Pro Glu Asp Ser Ser

-25 -20 -15

ccg gat gcc gcc cgc atc cga gtc aag cgc tac cgc cag agc atg aac 464

Pro Asp Ala Ala Arg Ile Arg Val Lys Arg Tyr Arg Gln Ser Met Asn

-10 -5 -1 1 5

aac ttc cag ggc ctc cgg agc ttt ggc tgc cgc ttc ggg acg tgc acg 512

Asn Phe Gln Gly Leu Arg Ser Phe Gly Cys Arg Phe Gly Thr Cys Thr

10 15 20

gtg cag aag ctg gca cac cag atc tac cag ttc aca gat aag gac aag 560

Val Gln Lys Leu Ala His Gln Ile Tyr Gln Phe Thr Asp Lys Asp Lys

25 30 35

gac aac gtc gcc ccc agg agc aag atc agc ccc cag ggc tac ggc cgc 608
 Asp Asn Val Ala Pro Arg Ser Lys Ile Ser Pro Gln Gly Tyr Gly Arg

40

45

50

cgg cgc cgg cgc tcc ctg ccc gag gcc ggc ccg ggt cgg act ctg gtg 656
 Arg Arg Arg Arg Ser Leu Pro Glu Ala Gly Pro Gly Arg Thr Leu Val

55

60

65

70

tct tct aag cca caa gca cac ggg gct cca gcc ccc ccg agt gga agt 704
 Ser Ser Lys Pro Gln Ala His Gly Ala Pro Ala Pro Pro Ser Gly Ser

75

80

85

gct ccc cac ttt ctt taggatitag gcgccaatgg tacaaggaat agtcgcgcaa 759
 Ala Pro His Phe Leu

90

gcattcccgct ggtgccctccc gggacgaagg acttcccgag cgggtgtgggg accgggctct 819

gacagccctg cggagaccct gattccggga ggcaccgtcc ggccggcgagc tctggctttg 879

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gatttctcac ggcgtgtcac cccaccaggg cgcaagcctc actattactt gaactttcca 1119

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<210> 2

<211> 185

<212> PRT

<213> Homo sapiens

<400> 2

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-90 -85 -80

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-75 -70 -65

Lys Trp Asn Lys Trp Ala Leu Ser Arg Gly Lys Arg Glu Leu Arg Met
-60 -55 -50

Ser Ser Ser Tyr Pro Thr Gly Leu Ala Asp Val Lys Ala Gly Pro Ala
-45 -40 -35

Gln Thr Leu Ile Arg Pro Gln Asp Met Lys Gly Ala Ser Arg Ser Pro
-30 -25 -20 -15

Glu Asp Ser Ser Pro Asp Ala Ala Arg Ile Arg Val Lys Arg Tyr Arg
-10 -5 -1 1

Gln Ser Met Asn Asn Phe Gln Gly Leu Arg Ser Phe Gly Cys Arg Phe
5 10 15

Gly Thr Cys Thr Val Gln Lys Leu Ala His Gln Ile Tyr Gln Phe Thr
20 25 30

Asp Lys Asp Lys Asp Asn Val Ala Pro Arg Ser Lys Ile Ser Pro Gln

35 40 45 50

Gly Tyr Gly Arg Arg Arg Arg Arg Ser Leu Pro Glu Ala Gly Pro Gly

55 60 65

Arg Thr Leu Val Ser Ser Lys Pro Gln Ala His Gly Ala Pro Ala Pro

70 75 80

Pro Ser Gly Ser Ala Pro His Phe Leu

85 90

<210> 3

<211> 1493

<212> DNA

<213> Sus scrofa

<220>

<221> CDS

<222> (148)..(711)

<220>

<221> mat peptide

<222> (430)..(585)

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tgccacigcc agagggacgt ctcagacttc atcttcccaa atcttggcag atcaccacct 120

tagcagggtc tgcacatctc agccggg atg aag ctg gtt ccc gta gcc ctc atg 174

Met Lys Leu Val Pro Val Ala Leu Met

-90

tac ctg ggc tgc ctc gcc ttc ctg ggc gct gac aca gct cgg ctc gac 222

Tyr Leu Gly Ser Leu Ala Phe Leu Gly Ala Asp Thr Ala Arg Leu Asp

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gtg gcg gca gag ttc cga aag aaa tgg aat aag tgg gct cta agt cgt	270			
Val Ala Ala Glu Phe Arg Lys Lys Trp Asn Lys Trp Ala Leu Ser Arg				
-65	-60	-55		
gga aaa aga gaa ctt cgg ctg tcc agc agc tac ccc acc ggg atc gcc	318			
Gly Lys Arg Glu Leu Arg Leu Ser Ser Ser Tyr Pro Thr Gly Ile Ala				
-50	-45	-40		
gac ttg aag gcc ggg cct gcc cag act gtc att cgg ccc cag gat gtg	366			
Asp Leu Lys Ala Gly Pro Ala Gln Thr Val Ile Arg Pro Gln Asp Val				
-35	-30	-25		
aag ggc tcc tct cgc agc ccc cag gcc agc att ccg gat gca gcc cgc	414			
Lys Gly Ser Ser Arg Ser Pro Gln Ala Ser Ile Pro Asp Ala Ala Arg				
-20	-15	-10		
atc cga gtc aag cgc tac cgc cag agt atg aac aac ttc cag ggc ctg	462			
Ile Arg Val Lys Arg Tyr Arg Gln Ser Met Asn Asn Phe Gln Gly Leu				
-5	-1	1	5	10
cgg agc ttc ggc tgt cgc ttt ggg acg tgc acc gtg cag aag ctg gcg	510			
Arg Ser Phe Gly Cys Arg Phe Gly Thr Cys Thr Val Gln Lys Leu Ala				
15	20	25		
cac cag atc tac cag ttc acg gac aaa gac aag gac ggc gtc gcc ccc	558			
His Gln Ile Tyr Gln Phe Thr Asp Lys Asp Lys Asp Gly Val Ala Pro				
30	35	40		
cgg agc aag atc agc ccc cag ggc tac ggc cgc cgg cgc cga cgc tct	606			
Arg Ser Lys Ile Ser Pro Gln Gly Tyr Gly Arg Arg Arg Arg Ser				
45	50	55		
ctg ccc gaa gcc agc ctg ggc cgg act ctg agg tcc cag gag cca cag	654			
Leu Pro Glu Ala Ser Leu Gly Arg Thr Leu Arg Ser Gln Glu Pro Gln				

60

65

70

75

gcg cac ggg gcc ccg gcc tcc ccg gcg cat caa gtg ctc gcc act ctc 702

Ala His Gly Ala Pro Ala Ser Pro Ala His Gln Val Leu Ala Thr Leu

80

85

90

ttt agg att taggcgccta ctgtggcagc agcgaacagt cgcgcatgca 751

Phe Arg Ile

tcatgccggc gcttcctggg gcggggggct tcccggagcc gagccctca gcggctgggg 811

ccccggcaga gacagcattg agagaccgag agtccgggag gcacagacca gcggcgagcc 871

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agaggtaact atcaataatt aagtgtgtg ctgtcaagat tttttttgt aacttcaaat 1231

atagagatat tttgtacgt tatatatgtg attaaggga ttttaaaca attgtattgt 1291

tcccccccc tctatitaa tatgtgaatg tctcagcgag gtgtaacatt gtttgcctgcg 1351

cgaaatgtga gagtgtgtgt gtgtgtgtgc gtgaaagaga gtctggatgc ctcttgggga 1411

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aaaccaataa actgtctcaa tg

1493

<210> 4

<211> 188

<212> PRT

<213> Sus scrofa

<400> 4

Met Lys Leu Val Pro Val Ala Leu Met Tyr Leu Gly Ser Leu Ala Phe

-90

-85

-80

Leu Gly Ala Asp Thr Ala Arg Leu Asp Val Ala Ala Glu Phe Arg Lys

-75

-70

-65

Lys Trp Asn Lys Trp Ala Leu Ser Arg Gly Lys Arg Glu Leu Arg Leu

-60

-55

-50

Ser Ser Ser Tyr Pro Thr Gly Ile Ala Asp Leu Lys Ala Gly Pro Ala

-45

-40

-35

Gln Thr Val Ile Arg Pro Gln Asp Val Lys Gly Ser Ser Arg Ser Pro

-30

-25

-20

-15

Gln Ala Ser Ile Pro Asp Ala Ala Arg Ile Arg Val Lys Arg Tyr Arg

-10

-5

-1 1

Gln Ser Met Asn Asn Phe Gln Gly Leu Arg Ser Phe Gly Cys Arg Phe

5

10

15

Gly Thr Cys Thr Val Gln Lys Leu Ala His Gln Ile Tyr Gln Phe Thr

20

25

30

Asp Lys Asp Lys Asp Gly Val Ala Pro Arg Ser Lys Ile Ser Pro Gln

35

40

45

50

Gly Tyr Gly Arg Arg Arg Arg Ser Leu Pro Glu Ala Ser Leu Gly

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60

65

Arg Thr Leu Arg Ser Gln Glu Pro Gln Ala His Gly Ala Pro Ala Ser
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Pro Ala His Gln Val Leu Ala Thr Leu Phe Arg Ile
85 90

<210> 5
<211> 1376
<212> DNA
<213> Rattus norvegicus

<220>
<221> CDS
<222> (154)..(708)

<220>
<221> mat peptide
<222> (433)..(582)

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cctttcagca gggtatcgga gcatcgctac aga atg aag ctg gtt tcc atc gcc 174
Met Lys Leu Val Ser Ile Ala
-90

ctg atg tta ttg ggt tcg ctc gcc gtt ctc ggc gcg gac acc gca cgg 222
Leu Met Leu Leu Gly Ser Leu Ala Val Leu Gly Ala Asp Thr Ala Arg
-85 -80 -75

ctc gac act tcc tcg cag ttc cga aag aag tgg aat aag tgg gcg cta 270
Leu Asp Thr Ser Ser Gln Phe Arg Lys Lys Trp Asn Lys Trp Ala Leu
-70 -65 -60 -55

agt cgt ggg aag agg gaa cta caa gcg tcc agc agc tac cct acg ggg	318
Ser Arg Gly Lys Arg Glu Leu Gln Ala Ser Ser Ser Tyr Pro Thr Gly	
-50 -45 -40	
ctc gtt gat gag aag aca gtc ccg acc cag act ctt ggg ctc cag gac	366
Leu Val Asp Glu Lys Thr Val Pro Thr Gln Thr Leu Gly Leu Gln Asp	
-35 -30 -25	
aag cag agc acg tct agc acc cca caa gcc agc act cag agc aca gcc	414
Lys Gln Ser Thr Ser Ser Thr Pro Gln Ala Ser Thr Gln Ser Thr Ala	
-20 -15 -10	
cac att cga gtc aaa cgc tac cgc cag agc atg aac cag ggg tcc cgc	462
His Ile Arg Val Lys Arg Tyr Arg Gln Ser Met Asn Gln Gly Ser Arg	
-5 -1 1 5 10	
agc act gga tgc cgc ttt ggg acc tgc aca atg cag aaa ctg gct cac	510
Ser Thr Gly Cys Arg Phe Gly Thr Cys Thr Met Gln Lys Leu Ala His	
15 20 25	
cag atc tac cag ttt aca gac aaa gac aag gac ggc atg gcc ccc aga	558
Gln Ile Tyr Gln Phe Thr Asp Lys Asp Lys Asp Gly Met Ala Pro Arg	
30 35 40	
aac aag atc agc cct caa ggc tat ggc cgc cgg cgc cgg cgt tcc ctg	606
Asn Lys Ile Ser Pro Gln Gly Tyr Gly Arg Arg Arg Arg Arg Ser Leu	
45 50 55	
cca gag gtc ctc cga gcc cgg act gtg gag tcc tcc cag gag cag aca	654
Pro Glu Val Leu Arg Ala Arg Thr Val Glu Ser Ser Gln Glu Gln Thr	
60 65 70	
cac tca gct cca gcc tcc ccg gcg cac caa gac atc tcc aga gtc tct	702
His Ser Ala Pro Ala Ser Pro Ala His Gln Asp Ile Ser Arg Val Ser	
75 80 85 90	

agg tta taggtgcggg tggcagcatt gaacagtcgg gcgagtatcc catlggcgcc 758
 Arg Leu

tgcggaatca gagagcttcg cacccigagc ggactigagc aatcttgag agatctgcct 818

ggctgcccct aggggaggca gaggaacca agatcaagcc aggtcacgt cagaaaccga 878

gaattacagg ctgatactct ctccgggcag gggctigagc cactgccttg cccgtcata 938

aactggtttt ctacggggc atacggctca ttacttactt gaactttcca aaacctagcg 998

agggaaagtg caatgcttgt lalacagcca aaggtaacta tcatatttaa gtttgtgat 1058

gtcaagaggt ttttttttt gtaacttcaa atatatagaa atatitttgt acgttatata 1118

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gtgtgtgtgt gtgtgtgtaa ggtggagagc gccigattac cgccigtgga tgaagaaaaa 1298

acattgtgtc ttctataatc tatttacata aaatatgtga tctgggaaaa agcaaaccaa 1358

taaactgtct caatgctg 1376

<210> 6

<211> 185

<212> PRT

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<400> 6

Met Lys Leu Val Ser Ile Ala Leu Met Leu Leu Gly Ser Leu Ala Val

-90

-85

-80

Leu Gly Ala Asp Thr Ala Arg Leu Asp Thr Ser Ser Gln Phe Arg Lys
-75 -70 -65

Lys Trp Asn Lys Trp Ala Leu Ser Arg Gly Lys Arg Glu Leu Gln Ala
-60 -55 -50

Ser Ser Ser Tyr Pro Thr Gly Leu Val Asp Glu Lys Thr Val Pro Thr
-45 -40 -35 -30

Gln Thr Leu Gly Leu Gln Asp Lys Gln Ser Thr Ser Ser Thr Pro Gln
-25 -20 -15

Ala Ser Thr Gln Ser Thr Ala His Ile Arg Val Lys Arg Tyr Arg Gln
-10 -5 -1 1

Ser Met Asn Gln Gly Ser Arg Ser Thr Gly Cys Arg Phe Gly Thr Cys
5 10 15

Thr Met Gln Lys Leu Ala His Gln Ile Tyr Gln Phe Thr Asp Lys Asp
20 25 30 35

Lys Asp Gly Met Ala Pro Arg Asn Lys Ile Ser Pro Gln Gly Tyr Gly
40 45 50

Arg Arg Arg Arg Arg Ser Leu Pro Glu Val Leu Arg Ala Arg Thr Val
55 60 65

Glu Ser Ser Gln Glu Gln Thr His Ser Ala Pro Ala Ser Pro Ala His
70 75 80

Gln Asp Ile Ser Arg Val Ser Arg Leu
85 90